



SEQUENCE LISTING

#6

<110> Farries, Timothy C.

Harrison, Richard A.

<120> Down-Regulation Resistant C3 Convertase

<130> 4-30443/A/IMU/PCT

<140> 09/142,334

<141> 1999-04-15

<150> PCT/GB97/00603

<151> 1997-03-04

<160> 35

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:

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oligodeoxynucleotide QRI1

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oligodeoxynucleotide QRI1n

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antisense oligodeoxynucleotide

QRI2n

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<223> Description of Artificial Sequence: primer

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<223> Description of Artificial Sequence: primer

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<223> Description of Artificial Sequence: mutagenic
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<212> DNA

<213> Homo sapiens

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<223> Description of Artificial Sequence: mutagenic

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<223> Description of Artificial Sequence: primer

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<211> 20

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<223> Description of Artificial Sequence: mutagenic

primer

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<211> 35

<212> DNA

<213> Homo sapiens

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<223> Description of Artificial Sequence: mutagenic
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<223> Description of Artificial Sequence: mutagenic
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<212> PRT

<213> Homo sapiens

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10

15

Leu Pro Leu Ala Leu Gly Ser Pro Met Tyr Ser Ile Ile Thr Pro Asn

20

25

30

Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu Glu Ala His Asp

35

40

45

Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His Asp Phe Pro Gly

50

55

60

Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu Thr Pro Ala Thr

65

70

75

80

Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala Asn Arg Glu Phe

85

90

95

Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val Gln Ala Thr Phe

100

105

110

Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser Leu Gln Ser Gly

115

120

125

Tyr Leu Phe Ile Gln Thr Asp Lys Thr Ile Tyr Thr Pro Gly Ser Thr

130

135

140

Val Leu Tyr Arg Ile Phe Thr Val Asn His Lys Leu Leu Pro Val Gly

145

150

155

160

Arg Thr Val Met Val Asn Ile Glu Asn Pro Glu Gly Ile Pro Val Lys

165

170

175

Gln Asp Ser Leu Ser Ser Gln Asn Gln Leu Gly Val Leu Pro Leu Ser

180

185

190

Trp Asp Ile Pro Glu Leu Val Asn Met Gly Gln Trp Lys Ile Arg Ala

195

200

205

Tyr Tyr Glu Asn Ser Pro Gln Gln Val Phe Ser Thr Glu Phe Glu Val

210

215

220

Lys Glu Tyr Val Leu Pro Ser Phe Glu Val Ile Val Glu Pro Thr Glu

225

230

235

240

Lys Phe Tyr Tyr Ile Tyr Asn Glu Lys Gly Leu Glu Val Thr Ile Thr

245

250

255

Ala Arg Phe Leu Tyr Gly Lys Lys Val Glu Gly Thr Ala Phe Val Ile

260

265

270

Phe Gly Ile Gln Asp Gly Glu Gln Arg Ile Ser Leu Pro Glu Ser Leu

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285

Lys Arg Ile Pro Ile Glu Asp Gly Ser Gly Glu Val Val Leu Ser Arg

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300

Lys Val Leu Leu Asp Gly Val Gln Asn Pro Arg Ala Glu Asp Leu Val

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315

320

Gly Lys Ser Leu Tyr Val Ser Ala Thr Val Ile Leu His Ser Gly Ser

325

330

335

Asp Met Val Gln Ala Glu Arg Ser Gly Ile Pro Ile Val Thr Ser Pro

340

345

350

Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met

355

360

365

Pro Phe Asp Leu Met Val Phe Val Thr Asn Pro Asp Gly Ser Pro Ala

370

375

380

Tyr Arg Val Pro Val Ala Val Gln Gly Glu Asp Thr Val Gln Ser Leu

385

390

395

400

Thr Gln Gly Asp Gly Val Ala Lys Leu Ser Ile Asn Thr His Pro Ser

405

410

415

Gln Lys Pro Leu Ser Ile Thr Val Arg Thr Lys Lys Gln Glu Leu Ser

420

425

430

Glu Ala Glu Gln Ala Thr Arg Thr Met Gln Ala Leu Pro Tyr Ser Thr

435

440

445

Val Gly Asn Ser Asn Asn Tyr Leu His Leu Ser Val Leu Arg Thr Glu

450

455

460

Leu Arg Pro Gly Glu Thr Leu Asn Val Asn Phe Leu Leu Arg Met Asp

465

470

475

480

Arg Ala His Glu Ala Lys Ile Arg Tyr Tyr Thr Tyr Leu Ile Met Asn

485

490

495

Lys Gly Arg Leu Leu Lys Ala Gly Arg Gln Val Arg Glu Pro Gly Gln

500

505

510

Asp Leu Val Val Leu Pro Leu Ser Ile Thr Thr Asp Phe Ile Pro Ser

515

520

525

Phe Arg Leu Val Ala Tyr Tyr Thr Leu Ile Gly Ala Ser Gly Gln Arg

530

535

540

Glu Val Val Ala Asp Ser Val Trp Val Asp Val Lys Asp Ser Cys Val

545

550

555

560

Gly Ser Leu Val Val Lys Ser Gly Gln Ser Glu Asp Arg Gln Pro Val

565

570

575

Pro Gly Gln Gln Met Thr Leu Lys Ile Glu Gly Asp His Gly Ala Arg

580

585

590

Val Val Leu Val Ala Val Asp Lys Gly Val Phe Val Leu Asn Lys Lys

595

600

605

Asn Lys Leu Thr Gln Ser Lys Ile Trp Asp Val Val Glu Lys Ala Asp

610

615

620

Ile Gly Cys Thr Pro Gly Ser Gly Lys Asp Tyr Ala Gly Val Phe Ser

625

630

635

640

Asp	Ala	Gly	Leu	Thr	Phe	Thr	Ser	Ser	Ser	Gly	Gln	Gln	Thr	Ala	Gln	645	650	655	
Arg	Ala	Glu	Leu	Gln	Cys	Pro	Gln	Pro	Ala	Ala	Arg	Arg	Arg	Arg	Ser	660	665	670	
Val	Gln	Leu	Thr	Glu	Lys	Arg	Met	Asp	Lys	Val	Gly	Lys	Tyr	Pro	Lys	675	680	685	
Glu	Leu	Arg	Lys	Cys	Cys	Glu	Asp	Gly	Met	Arg	Glu	Asn	Pro	Met	Arg	690	695	700	
Phe	Ser	Cys	Gln	Arg	Arg	Thr	Arg	Phe	Ile	Ser	Leu	Gly	Glu	Ala	Cys	705	710	715	720
Lys	Lys	Val	Phe	Leu	Asp	Cys	Cys	Asn	Tyr	Ile	Thr	Glu	Leu	Arg	Arg	725	730	735	
Gln	His	Ala	Arg	Ala	Ser	His	Leu	Gly	Leu	Ala	Arg	Ser	Asn	Leu	Asp	740	745	750	
Glu	Asp	Ile	Ile	Ala	Glu	Glu	Asn	Ile	Val	Ser	Arg	Ser	Glu	Phe	Pro	755	760	765	
Glu	Ser	Trp	Leu	Trp	Asn	Val	Glu	Asp	Leu	Lys	Glu	Pro	Pro	Lys	Asn	770	775	780	
Gly	Ile	Ser	Thr	Lys	Leu	Met	Asn	Ile	Phe	Leu	Lys	Asp	Ser	Ile	Thr	785	790	795	800

Thr Trp Glu Ile Leu Ala Val Ser Met Ser Asp Lys Lys Gly Ile Cys

805

810

815

Val Ala Asp Pro Phe Glu Val Thr Val Met Gln Asp Phe Phe Ile Asp

820

825

830

Leu Arg Leu Pro Tyr Ser Val Val Arg Asn Glu Gln Val Glu Ile Arg

835

840

845

Ala Val Leu Tyr Asn Tyr Arg Gln Asn Gln Glu Leu Lys Val Arg Val

850

855

860

Glu Leu Leu His Asn Pro Ala Phe Cys Ser Leu Ala Thr Thr Lys Arg

865

870

875

880

Arg His Gln Gln Thr Ile Thr Ile Pro Pro Lys Ser Ser Leu Ser Val

885

890

895

Pro Tyr Val Ile Val Pro Leu Lys Thr Gly Leu Gln Glu Val Glu Val

900

905

910

Lys Ala Ala Val Tyr His His Phe Ile Ser Asp Gly Val Arg Lys Ser

915

920

925

Leu Lys Val Val Pro Glu Gly Ile Arg Met Asn Lys Thr Val Ala Val

930

935

940

Arg Thr Leu Asp Pro Glu Arg Leu Gly Arg Glu Gly Val Gln Lys Glu

945

950

955

960

Asp Ile Pro Pro Ala Asp Leu Ser Asp Gln Val Pro Asp Thr Glu Ser

965

970

975

Glu Thr Arg Ile Leu Leu Gln Gly Thr Pro Val Ala Gln Met Thr Glu

980

985

990

Asp Ala Val Asp Ala Glu Arg Leu Lys His Leu Ile Val Thr Pro Ser

995

1000

1005

Gly Cys Gly Glu Gln Asn Met Ile Gly Met Thr Pro Thr Val Ile Ala

1010

1015

1020

Val His Tyr Leu Asp Glu Thr Glu Gln Trp Glu Lys Phe Gly Leu Glu

1025

1030

1035

1040

Lys Arg Gln Gly Ala Leu Glu Leu Ile Lys Lys Gly Tyr Thr Gln Gln

1045

1050

1055

Leu Ala Phe Arg Gln Pro Ser Ser Ala Phe Ala Ala Phe Val Lys Arg

1060

1065

1070

Ala Pro Ser Thr Trp Leu Thr Ala Tyr Val Val Lys Val Phe Ser Leu

1075

1080

1085

Ala Val Asn Leu Ile Ala Ile Asp Ser Gln Val Leu Cys Gly Ala Val

1090

1095

1100

Lys Trp Leu Ile Leu Glu Lys Gln Lys Pro Asp Gly Val Phe Gln Glu

1105	1110	1115	1120
Asp Ala Pro Val Ile His Gln Glu Met Ile Gly Gly Leu Arg Asn Asn			
1125	1130	1135	
Asn Glu Lys Asp Met Ala Leu Thr Ala Phe Val Leu Ile Ser Leu Gln			
1140	1145	1150	
Glu Ala Lys Asp Ile Cys Glu Glu Gln Val Asn Ser Leu Pro Gly Ser			
1155	1160	1165	
Ile Thr Lys Ala Gly Asp Phe Leu Glu Ala Asn Tyr Met Asn Leu Gln			
1170	1175	1180	
Arg Ser Tyr Thr Val Ala Ile Ala Gly Tyr Ala Leu Ala Gln Met Gly			
1185	1190	1195	1200
Arg Leu Lys Gly Pro Leu Leu Asn Lys Phe Leu Thr Thr Ala Lys Asp			
1205	1210	1215	
Lys Asn Arg Trp Glu Asp Pro Gly Lys Gln Leu Tyr Asn Val Glu Ala			
1220	1225	1230	
Thr Ser Tyr Ala Leu Leu Ala Leu Leu Gln Leu Lys Asp Phe Asp Phe			
1235	1240	1245	
Val Pro Pro Val Val Arg Trp Leu Asn Glu Gln Arg Tyr Tyr Gly Gly			
1250	1255	1260	

Gly Tyr Gly Ser Thr Gln Ala Thr Phe Met Val Phe Gln Ala Leu Ala

1265 1270 1275 1280

Gln Tyr Gln Lys Asp Ala Pro Asp His Gln Glu Leu Asn Leu Asp Val

1285 1290 1295

Ser Leu Gln Leu Pro Ser Arg Ser Ser Lys Ile Thr His Arg Ile His

1300 1305 1310

Trp Glu Ser Ala Ser Leu Leu Arg Ser Glu Glu Thr Lys Glu Asn Glu

1315 1320 1325

Gly Phe Thr Val Thr Ala Glu Gly Lys Gly Gln Gly Thr Leu Ser Val

1330 1335 1340

Val Thr Met Tyr His Ala Lys Ala Lys Asp Gln Leu Thr Cys Asn Lys

1345 1350 1355 1360

Phe Asp Leu Lys Val Thr Ile Lys Pro Ala Pro Glu Thr Glu Lys Arg

1365 1370 1375

Pro Gln Asp Ala Lys Asn Thr Met Ile Leu Glu Ile Cys Thr Arg Tyr

1380 1385 1390

Arg Gly Asp Gln Asp Ala Thr Met Ser Ile Leu Asp Ile Ser Met Met

1395 1400 1405

Thr Gly Phe Ala Pro Asp Thr Asp Asp Leu Lys Gln Leu Ala Asn Gly

1410 1415 1420

Val Asp Arg Tyr Ile Ser Lys Tyr Glu Leu Asp Lys Ala Phe Ser Asp

1425 1430 1435 1440

Arg Asn Thr Leu Ile Ile Tyr Leu Asp Lys Val Ser His Ser Glu Asp

1445 1450 1455

Asp Cys Leu Ala Phe Lys Val His Gln Tyr Phe Asn Val Glu Leu Ile

1460 1465 1470

Gln Pro Gly Ala Val Lys Val Tyr Ala Tyr Tyr Asn Leu Glu Glu Ser

1475 1480 1485

Cys Thr Arg Phe Tyr His Pro Glu Lys Glu Asp Gly Lys Leu Asn Lys

1490 1495 1500

Leu Cys Arg Asp Glu Leu Cys Arg Cys Ala Glu Glu Asn Cys Phe Ile

1505 1510 1515 1520

Gln Lys Ser Asp Asp Lys Val Thr Leu Glu Glu Arg Leu Asp Lys Ala

1525 1530 1535

Cys Glu Pro Gly Val Asp Tyr Val Tyr Lys Thr Arg Leu Val Lys Val

1540 1545 1550

Gln Leu Ser Asn Asp Phe Asp Glu Tyr Ile Met Ala Ile Glu Gln Thr

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Ile Lys Ser Gly Ser Asp Glu Val Gln Val Gly Gln Gln Arg Thr Phe

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Ile Ser Pro Ile Lys Cys Arg Glu Ala Leu Lys Leu Glu Glu Lys Lys
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His Tyr Leu Met Trp Gly Leu Ser Ser Asp Phe Trp Gly Glu Lys Pro
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Asn Leu Ser Tyr Ile Ile Gly Lys Asp Thr Trp Val Glu His Trp Pro
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Leu Gly Ala Phe Thr Glu Ser Met Val Val Phe Gly Cys Pro Asn
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<212> DNA

<213> Homo sapiens

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His His His His His His

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5

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5

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5

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